

# **EXHIBIT B**

Alignment of nucleotide sequences of glutamine synthetase genes

	1	50
2247	(1) -----GTGGCGTTGAA-----ACCCCGGAAGAAATTGTCAAGTT	
13032	(1) -----GTGGCGTTGAA-----ACCCCGGAAGAAATTGTCAAGTT	
CEFgInA1	(1) -----GTGGCGTTAAC-----ACCCCGGAAGAAAGTAAACCAAGTT	
CEFgInA2	(1) -----GTGGCCTCGAGCCCCGACAACCAAACCGGATGAGAATCCTCAAGTT	
MtugInA2	(1) -----ATGGACCGAGAGAAGGAATTCTGTTCTTCG	
MtugInA3	(1) -----ATGACAGCCACACCGCTTCCC GGCCCGCAT	
MtugInA4	(1) GTGACCCGGCCCCGGTTCGCCGCCGTTGGCTGGGACCGAGTTGGAGCGAC	
MtugInA1	(1) -----GTGACGGAAAGACGCCGACGACGCTCTCAAAC	
Consensus	(1) -----GTGGCGGATGAACCCCGGA GAA T GTCAAGTT	
	51	100
2247	(36) CATCAAGGATGAA-----AACGTCGAGTTCTGACGTTCGATTACCCG	
13032	(36) CATCAAGGATGAA-----AACGTCGAGTTCTGACGTTCGATTACCCG	
CEFgInA1	(36) CATCAAGGATGAA-----AACGTTGAGTTCTGTCGATGTCGATTACCCG	
CEFgInA2	(45) CATCCGGGACAATTGACATTCGCTTCGTCGGCTGGGTTACACAG	
MtugInA2	(30) TACCC-----TGGAAAGAACGCGACATTCGCTTCGTCGGCTGGGTTACACAG	
MtugInA3	(33) CGCCCAATTGGAGGCAGAGGGCTGACACCGTCATCGGACCGTCTGTA	
MtugInA4	(51) GGTCG-----GACGCCGATCGTCCGCTTCACCC	
MtugInA1	(36) TGCCAAGGACGAG-----AAGTCGAATATGTCGACGTCGGGTTCTGTC	
Consensus	(51) CATCAAGGATGAA-----GACGTCGACTTCGTCGACGTCGGGTTACCCG	
	101	150
2247	(80) ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT	
13032	(80) ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT	
CEFgInA1	(80) ACCTTCCCGGAATCGAGCAGCACTTCAGCATCCCCGCACTCGCTCTGAT	
CEFgInA2	(89) ACGTTCCCGGCACCGAATCGAGCAGCACTTCAGCATCCCCGCACTCGCTCTGAC	
MtugInA2	(77) ACGTGTGGTTTCCTCAAGTCGGCTGGCCATCGGCCCAGGGAACTCGA	
MtugInA3	(83) ACCCCGGCGGACTCACCCAGGCCAAGACCGTGCGGATAACCCGGACCAA	
MtugInA4	(95) ACAATGAGGGC-----GGCTGGCGGCCAACGGATAACGGGCGGCA	
MtugInA1	(80) ACCTGCTGGCATCATCGAGCACTTCAGCATTCGGGTTGGGCTTGTGAC	
Consensus	(101) ACCTTCCCGGCATCGAGCAGCACTTCAGCATCCCAGCCGGCTTCGA	
	151	200
2247	(130) GCAGATAACAGTCGAAAGGGCTCGCACTCGACGGATCCCTCGATCCGGTGG	
13032	(130) GCAGATAACATCGAAGAAGGCTCGCATTTCGACGGATCCCTCGATCCGGTGG	
CEFgInA1	(130) GAGGAGCCOCATCGAGGAGGGCTCCCTTCGACGGTTCCCTCCATCCGGTGG	
CEFgInA2	(139) GAATCCCGCATGGAAAACGGACTCGGCTTCGACGGGTCACTGATCAGCGG	
MtugInA2	(126) GGGGCCCTTCGAGGAAGGCATCGGCTTCGACGGATCCCTCGATCGAGGG	
MtugInA3	(132) CACATTGCGCAA-----TCCTGGCTTGGCCAGTCCGGTGTGGCA	
MtugInA4	(138) T-----TTCGTCACGACATAGCCACCCGGCGTCAAGTGTGCTGCAG	
MtugInA1	(130) AAGAGGGTGTGTTGACGACGGCTTCGGCTTGTGACGGCTCGTCGATTGGCG	
Consensus	(151) G G CGC TTCGA GA GGCCTCGCCCTCGACGGTCCTCGATCCGGGG	
	201	250
2247	(180) CTTCACCAACGATCGAGGAATCTGACATGAACTCTCTGCCAGACCTC-GGA	
13032	(180) CTTCACCAACGATCGAGGAATCTGACATGAACTCTCTGCCAGACCTC-GGA	
CEFgInA1	(180) TTTCACCAACATGAAATCGGACATGAACTCTGCTGCCGGATCTG-GCC	
CEFgInA2	(189) ATACACCACTGTCGACGGATTCGGACATGATGCTGCTGCCGGATCTG-TCC	
MtugInA2	(174) CTTTGGCGGGTCTCCGAATCGGATACGGTGGCGACCCGGACCC	
MtugInA3	(174) TACGTTGTTGACGACGATGCACTTGTGATCACCAGAACATCAGTG	
MtugInA4	(180) TTATCTGCTGGCCGTCGACGTTGACGCTGAAACGGTGGCCGGCTAT-GCG	
MtugInA1	(180) GTTCCAGTCGATCCACGAATCGGACATGTTGCTCTTCCCAGATGCC-GAG	
Consensus	(201) TTTCACCAACGATCGAGGAATCGGACATGAACTCTCTGCCAGACCTC-GGA	
	251	300

2247	(229)	ACGGCCACCCCTTGTATCC	ATTCCCGCAA	GGCAAGACCTGAACTG
13032	(229)	ACGGCCACCCCTTGTATCC	ATTCCCGCAA	GGCAAGACCTGAACTG
CEFgInA1	(229)	ACCGCGAAGATCGATCC	GTTCCGCAGA	GGCGAAGACCTGAACTG
CEFgInA2	(238)	ACCGCGTTCATCGACCC	GTTCCGCAGA	GTCGAAGACCTGAACTG
MtugInA2	(218)	CGTCGACCTTCCAGGT	GCTGCCCTG	GGCCAAC
MtugInA3	(224)	TGGTCGGCAGTCAACGT	CTCCGCAT	CGAATC
MtugInA4	(229)	ATGGCCAGTTGGGACACCGGCTACGGCGATA	GGTGATGACGCCGGACT	
MtugInA1	(229)	ACGGGCCGATCGACCC	GTTCCGCAC	GGCGAAGACCTGAACTG
Consensus	(251)	ACGGCGACCATCGACCC	GTTCCGCAC	GGCGAAGACCTGAACTG
	301			350
2247	(273)	-TAAGTTCTTCGTTACGATCC	TTTACCCCCGAGGCATTC	CTCCCGCGAC
13032	(273)	-TAAGTTCTTCGTTACGATCC	TTTACCCCCGAGGCATTC	CTCCCGCGAC
CEFgInA1	(273)	-CAAGTTCTTCGTCCTAACGATCC	TTTACCCCCGAGGCATTC	CTCCCGCGAC
CEFgInA2	(282)	-CAAGTTCTTCGTCCTAACGATCC	TTTACCCCCGAGGCATTC	CTCCCGCGAC
MtugInA2	(250)	-AGTTCCGGCCATTGGGCA	TTTACCCCCGAGGCATTC	CTCCCGCGAC
MtugInA3	(254)	-TGTCCGCCTTGGGCA	TTTACCCCCGAGGCATTC	CTCCCGCGAC
MtugInA4	(279)	GTCCACTCTGGGCTGATT	TTTACCCCCGAGGCATTC	CTCCCGCGAC
MtugInA1	(273)	-CAACTCTTTEGACGACCCCTTACCCCTGGAGCGT	TTTACCCCCGAGGCATTC	CTCCCGCGAC
Consensus	(301)	TAAGTTCTTCGTCCTAACGATCC	TTTACCCCCGAGGCATTC	CTCCCGCGAC
	351			400
2247	(322)	CCACGGCAACGTAGGACCGAAGGCAGAGCAGTACCTGGC	ATCCACCGG	
13032	(322)	CCACGGCAACGTGGCACCGAAGGCAGAGCAGTACCTGGC	ATCCACCGG	
CEFgInA1	(322)	CCCCCGCAATGTTGGCACCGTAAAGGCCGAGCAGTACCTGGC	ATCCACCGG	
CEFgInA2	(331)	CCCCCGCAACATCGCCCGCAAGGGGGAGGAGTACCTGGC	ATCCACCGG	
MtugInA2	(293)	CCATGGCGGACGGCTGGCC	ATCCACCGG	
MtugInA3	(299)	CCGGGTTTCTTCGAGCAGGACGGCACACCGGTCCCCCGC	ATCCACCGG	
MtugInA4	(329)	CCGACCTGGCTCTGGGCCACGGCAGCGAGGTGGCCGT	ATCCACCGG	
MtugInA1	(322)	CCCGCGAACATCGCCCGCAAGGGGGAGGAACTACCTGAT	ATCCACCGG	
Consensus	(351)	CC CGCAAC TGGC CGCAAGGCAGAGCAGTACCTGGC	ATCCACCGG	
	401			450
2247	(369)	CATTGGCACACCTGCAACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
13032	(369)	CATTGGCACACCTGCAACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
CEFgInA1	(369)	CATGGCGCACACCTGCAACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
CEFgInA2	(378)	TTTCGCGCACAGCTGTACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
MtugInA2	(337)	TTGGGGGGGACCTGAGGAAGGC		
MtugInA3	(345)	AGGAACACTGAGCGGATCGAGGCCGGCTTGTGTGATGCGGGCACTGGACG		
MtugInA4	(379)	ATTCTCGCCCGTCAGTCGATCGGCTCAAGGC		
MtugInA1	(369)	CATCGCGCACACCGCATACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
Consensus	(401)	CATCGCCGACACCTGCAACTTCGGGGGGAGGCTGAGTCTACCTCTTCG		
	451			500
2247	(419)	ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTCTACGAAGTAGAT		
13032	(419)	ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTCTACGAAGTAGAT		
CEFgInA1	(419)	ACTCCGTCCGTTACTCCACCGAGATGAACTCCGGCTTCTACGAAGTAGAT		
CEFgInA2	(428)	ACTCCGTGGGTTCAAGCTCCAGTCGAATCGGGCTTCCACGAGGTGGAT		
MtugInA2	(380)	GCTACGTGCATCCCGAAATCGAG		
MtugInA3	(395)	CGGTAACTGGGCCACGGAGTCGAA		
MtugInA4	(425)	CGATGTCGGGCCACGGAGCTGGAGTTCATCGT		
MtugInA1	(419)	ATTGGGTGAGCTTCGACTCGCGCGCCACGGCTCCCTCTACGAGGTGGAC		
Consensus	(451)	ACTCCGTGCCTACGACACCGAGTCAACCCCG	CCGTTCTACGAGGTGGAT	
	501			550
2247	(469)	ACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAAGCTGGACGGAC		

13032	(469)	ACCGAAGAAAGGCTGGTGGAACCGTGGCAAGGAAACCAACCTCGACGGCAC	
CEFgInA1	(469)	ACCAACGAGGGTTGGTGGAACCGTGGCCGTGAGACCAACCTCGATGGCAC	
CEFgInA2	(478)	TCCGTGGAGGGCTGGTGGAACAGTGGTTCCCGGGAGAACCGGACGGCAG	
MtugInA2	(418)	CCC-----GGACCGAGGACGGG-----TCGGTGCCCC	
MtugInA3	(433)	GCGGA-----C-----G-GCCACGGCTGCCT-----TCGAGG-CTG	
MtugInA4	(472)	CGCC-----AGGCA-----TGGGCCAGCGG-----GTA-----TCGCGGGCTG	
MtugInA1	(469)	GCCATCTCGGGGTTGGTGGAACACC GGCGCGACGGAGGCCGACGGCAG	
Consensus	(501)	CCGA GAGGGCTGGTGGAACCGTGGC GGA ACCAACCTCGACGGCAG	
	551		600
2247	(519)	CCC AAACCTGGGGGCAAAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG	
13032	(519)	CCC AAACCTGGGGGCAAAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG	
CEFgInA1	(519)	CCCCAACACCGGTTCCAAGAACCGCCTCAAGGGCGGTACTTCCCAGTCG	
CEFgInA2	(528)	CAGGAACCTGGTACAAGGTACGCCAGAACGGGTGGTACTTCCCAGTGG	
MtugInA2	(446)	TCCC-----GGTGG-----A-----CAACGCCGCTATTTCGACCAAG	
MtugInA3	(463)	T-----GGGC-----GC-----AGTACGG-----TGTGGCCGGGG	
MtugInA4	(505)	ACCC-----C-----GGGC-----AGCGA-----CTACAAACATCGACTACGGCATATTGG	
MtugInA1	(519)	TCCCAACCGGGGTTACAAGGTCCGCACAAAGGGGGGTATTTCAGCTGG	
Consensus	(551)	CCCCAACCGGGG AAG CGGC CAAGGGGGGTACTTCCCAGTGG	
	601		650
2247	(569)	CA---CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGGAACC	
13032	(569)	CA---CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGCAACC	
CEFgInA1	(569)	CA---CCCTACGACCAAGCCGTGGACGTGCGCGATGACATGGTCCGCAACC	
CEFgInA2	(578)	CA---CCCTATGACCACTTCCAGGACCTGGCGACACCCATTGGTGAGACCC	
MtugInA2	(479)	CG-----GTGACGACTCCGCCCTTGAACCTTGGCCGCCACGGATCGATGCC	
MtugInA3	(488)	TG-----CTCGAGGAGGAGGGTTCG-----TCGGCGATGTCAACCCCCGGCAA	
MtugInA4	(545)	CATCCTCGGGATGGAGCCGTTG-----CTGGCGACATCGGTGTTGGTA	
MtugInA1	(569)	CC-----CCCACGACCAATACTCGTGACCTGGCGGACAAGATGCTGACCAACC	
Consensus	(601)	CA CCCTACGACCAA CGGT GAC TGCGCGATGACATGGT GGCAACC	
	651		700
2247	(617)	TGGCAGCTTCCGGCTTCGGCTCTTGGCGTTTCCACCAACGAAGTCGG-----T	
13032	(617)	TGGCAGCTTCCGGCTTGGCTCTTGGCGTTTCCACCAACGAAGTCGG-----T	
CEFgInA1	(617)	TGGCGTGAAGCGGGTTTCCACCTGGAGCGTTTCCACCAACGAAGTCGG-----T	
CEFgInA2	(626)	TGGCGGGAGATCGGGTTCACCGTGGAGCGTTCCACCAATGAGATGGCCAGI	
MtugInA2	(527)	TGGAAATTCTATCGGCATCTCGGTGGAGTTAGCCCATCACGAAGGGCC-----A	
MtugInA3	(533)	CGGGCAG-----CAGGCATCGCTATCGAGCGATTCACCATCCGAATAACGG-----I	
MtugInA4	(590)	TGGCGGGTGGGGTCTGGGATCGGATTCAGGGCGGCAAAAGGGAAATGCAA-----C	
MtugInA1	(617)	TGATCAACTCCGGCTTCTATCTGGAGAAGGGCCACCAAGGGTGGGGCAGC	
Consensus	(651)	TGGCAG CCGGCTTC C CTGGAGCGTTTCCACCAACGAAGTCGG T	
	701		750
2247	(664)	GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCAATGCTCCACGGGGC	
13032	(664)	GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCAATGCTCCACGGGGC	
CEFgInA1	(664)	GGCGGCCACAGCAGGAGATCAACTACCGCTTCAACACCCATGCTCCACGGGGC	
CEFgInA2	(676)	GCTGGTCAGCAGGAGATCAACTACCGCTTCAACACCCATGCTCCACGGGGCAGC	
MtugInA2	(574)	CCCGGCCACAGCAGGAGATCAACTACCGCTTCAACACCCATGCTCCACGGGGC	
MtugInA3	(577)	GCCAAACCAATTGAGATCTGTTAGGCCCGCAGCCTGGTGGGGCTGGGGCCGC	
MtugInA4	(637)	ATGGGGCACAGCAGGAGATCGGTTCTGGCTACGACGAGGGCGCTGGTCAACCTG	
MtugInA1	(667)	GGCGGACAGCAGGAGATCAACTACCAAGTCAATTGGTGGCTGCAGGGCCGC	
Consensus	(701)	GGCGGCCACAGCAGGAGATCAACTACCG TTCAACACCCATGCTGCACGC GC	
	751		800
2247	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTGGCTCC	
13032	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTGGCTCC	

CEFgInA1	(714)	CGATGACATTCAAGACCTTCAGTACATCGTAAGAACACCCGCAGCCGTGC
CEFgInA2	(726)	CGATGACCTCCAGACCTTCAGTACGTGGTAAGAACACCGCGAAGGCCG
MtugInA2	(624)	TGACAACGTTGATGACCTTCAGCCTACGTCATCAAAGAAGTCGGCTGTTGAAG
MtugInA3	(627)	CGATCAGCTGGTCTGACCCGCCTCATCATGGCCGTACCGCCCGCCGGC
MtugInA4	(687)	CGACAACCATGCATCTACAAGAACGGCGCCAGGAAATCGCCGACCGAGC
MtugInA1	(717)	CGACGACATGCAGTTGACAGTACATCATCAAGAACACCCGCTGGCAGA
Consensus	(751)	CGATGACAT CAGACCTTCAGTACATCATCAAGAACACCCGC CGCC GC
	801	850
2247	(764)	ACGGCAAGGCTGCAACCTTCATGCCAAGGCCACTGGCTGGCGACAAACGGT
13032	(764)	ACGGCAAGGCTGCAACCTTCATGCCAAGGCCACTGGCTGGCGACAAACGGT
CEFgInA1	(764)	ACGGCAAGGCTGCAACCTTCATGCCAAGGCCACTGGCTGGCGACAAACGGC
CEFgInA2	(776)	TGGTAAATCCGCCACCTTCATGCCAAGGCCCTGGCTGGTGATGACGGCGGT
MtugInA2	(674)	AGGGCGCCGGCGCTGCTCATGCCAAGGCCATTCGCCAGCACCCGGC
MtugInA3	(677)	ACGGGTTACGCCATGAGCTATGCCAGGCCCTTCGCCGGAAAGTATCGGA
MtugInA4	(737)	ACGGCAAGAGCCTAACGTTCATGGCGAAATAACGATGAAACCCGAAGGT
MtugInA1	(767)	ACGGCAAAACGGCTCACGTTCATGCCAAGGCCGTGTCGGCGACAAACGGG
Consensus	(801)	ACGGCAAG C GC ACCTTCATGCCAAGCCACTGGCTGG GACAACGGT
	851	900
2247	(814)	TCCGGCATGCACGCTCACCAAGTCCCCTCTGGAAAGGACGGCAAGCCACT
13032	(814)	TCCGGCATGCACGCTCACCAAGTCCCCTCTGGAAAGGACGGCAAGCCACT
CEFgInA1	(814)	TCCGGCATGCACGCCACCAAGTCCCCTCTGGAAAGGACGGCAAGCCACT
CEFgInA2	(826)	TCCGGCATGGACATCCACCAAGTCGCTGTGGAAAGGACGGCAAGCCCT
MtugInA2	(724)	TCCGGCATGACACCCACATGAGCTGTCTGAGGGGTGATGTCACCGGTT
MtugInA3	(727)	TCCGGTGGCCACCAACACTTCTGGCTGACTATGTCGGAAAGGGATGCT
MtugInA4	(784)	AATAGCTGTACATCCATGTCGCTGCTGGCACGGATGGCTCCGGGT
MtugInA1	(817)	TCCGGCATGCACGTGTCATCAGTCGCTGTCGGAAAGGACGGGGCCCGCT
Consensus	(851)	TCCGGCATGCAC CCCACCAAGTCGCTGTGGAAAGG ACGGCAAGCCGCT
	901	950
2247	(861)	CTTCCACCGATGA-GTCCGGCTACGCAGGCCCTGTCCGACATCGCCGGCTAC
13032	(861)	CTTCCACCGATGA-GTCCGGCTACGCAGGCCCTGTCCGACATCGCCGGCTAC
CEFgInA1	(861)	CTTCCACCGATGA-GTCCGGCTACGCAGGCCCTGTCCGACATCGCCGGTTAC
CEFgInA2	(873)	CTTCCATGATGA-GGCCGGTTATGCCAACCTGTCCGGAGATGGCCCGTCAC
MtugInA2	(774)	CCACAGCCGTGATGAIICCGCT-GCAG-CTGTCGGAAAGTGGGTAAATCG
MtugInA3	(774)	CTTCTCCGGTGG-GACTGGAGCAGCTGGCATGACCTCGGCCGGGGAGGCC
MtugInA4	(834)	GTTGCCCCAGTAACGGGCGCAGG-CATGTCGCTGATGTTCCGCAGC
MtugInA1	(864)	GAATGTCAGGAGA-GACGGGTTATGCCGGTCTGTCGGACACGGCCCGTCAT
Consensus	(901)	CTTCCACCGATGA GACCGCTACGC GGCCGTGGACATGGCCCG TAC
	951	1000
2247	(910)	TACATCGGCCGCATCCGCCACACGGAGGCCGTGTCTGGCGTT-CACCA
13032	(910)	TACATCGGCCGCATCCGCCACACGGAGGCCGTGTCTGGCGTT-CACCA
CEFgInA1	(910)	TACATCGGTGGCATCCTGCCACACGGCGGTGGCTCTGGCGTT-CACCA
CEFgInA2	(922)	TATGTCGGTGGTCGCAAGCATGCCCGCCGGCTCTGGCGTT-CACCA
MtugInA2	(820)	TACATGCCGGGATCCTGGAGCACGGTGGCAGATCAGCGCGGT-CACAA
MtugInA3	(823)	GCGGTGGCAGGAGTGCTTC-GCGGAATACCGGACGCCAAGGCATCCTGT
MtugInA4	(883)	TTCGTCGGGGCCAGTGG-CCACGTTGCGCGAAATCACCGCTGCTATG
MtugInA1	(913)	TACATCGGGGCCGTCGCAACACGGGCCGTGGCGCGTT-CACCA
Consensus	(951)	TACATCGGCCGCATGCTGCCACACGGAGGCCGTCTGGCGTT CACCA
	1001	1050
2247	(959)	ACGGCAACCTGAACCTCCACCAACGGCTGGTTCGAGGCTGGACGGCTCCA
13032	(959)	ACGGCAACCTGAACCTCCACCAACGGCTGGTTCGAGGCTGGACGGCTCCA
CEFgInA1	(959)	ACCCGACCCCTGAACCTCCACCATGCCCTGGTGGCGCTGGCTTCGAGGCCCC

CEFgInA2	(971)	ACCCGACCCCTGAATCCTTACAACCGCTTGCTGCCGGTTCGAGGGCCCG
MtugInA2	(869)	ATCACTGGGTCAACTCTTACAAGCGGCTGGTGCAGGGCGCGAAGCGCCC
MtugInA3	(872)	GCGGATCGATCGTGTCCGGCTGCGAACTGGACCCGGTAAGTGGCGGGA
MtugInA4	(932)	CGCCGACCAATTAACTCTACAAAGCGATACTCCGATAGCAGTTCGCCCG
MtugInA1	(962)	ACCCGACGGTGAACTCTACAAAGCGGCTGGTTCGGTTACGAGGGCCCG
Consensus	(1001)	ACCCGACCCCTGAACTCTTACCGCGCTGGTCCGGTACGGAGGGCCCC
	1051	
2247	(1009)	ATCAACCTGGTGTACTCAACCGCTCCGCTGCTGTCGGTATCCC
13032	(1009)	ATCAACCTGGTGTACTCAACCGCTCCGCTGCTGTCGGTATCCC
CEFgInA1	(1009)	ATCAACCTGGTGTACTCCACAGCGCAACCGCTCCGCGCGTGGCTATCCC
CEFgInA2	(1021)	GTGAGCCCTGGCGTATTTCGGAGAGAACCGTCCGGCGGATCGGCATTCG
MtugInA2	(919)	ACGGCCGCGCTGCTGGGGGCCAACCGATCCGCCCTAGTGGCGGTGCC
MtugInA3	(922)	ATGATGCACTGCTGGGTACCGAAAACCGGGAAAGCGGGGTGGCATTCGT
MtugInA4	(982)	ACGGCGCTGGCTGGGGCTGGACAAATCCACCTGGCCCTGGGGTGG--
MtugInA1	(1012)	ATCAACCTGGTGTAGCCAGCGAACCGGCTGGCATGGCTGGCGATTCCT
Consensus	(1051)	ATCAACCTGGTGTAGCCAGCGAACCGGCTGGCATGGCTGGCGATTCCT
	1101	
2247	(1059)	AATCACCGGATCCAACCCAAAGGCAAGCGCATCGAATTCCGGCTC
13032	(1059)	AATCACCGGATCCAACCCGAAGGCAAGCGCATCGAATTCCGGCTC
CEFgInA1	(1059)	GATCACCGGTTCCAACCCGAAGGCAAGCGCATCGAGTTCCGGCAC
CEFgInA2	(1071)	GGCAGCGGTTCCAACCCGAAGGCAAGCGCATCGAGTTCCGGCAC
MtugInA2	(969)	GATGTACACGCCAACAGACCTCGTGGCGGGGGTCAAAGTAGCCAGG
MtugInA3	(972)	CAAGGGCGGGCTGGTACCGGGTACCGGGGGAAACGTCGAGGTGAAGGTCG
MtugInA4	(1030)	GTGGCCACGGGCAAAACATC---CGGGTCAAATGGCCGGTT
MtugInA1	(1062)	GATCACCGGAGCAACCCGAAGGCAAGCGCATGGAGTTCCGAAAGG
Consensus	(1101)	GATCACCGGCCAACCCGAAGGCAAGCGCATCGAGTTCCGGCGCC
	1151	
2247	(1106)	CAGACCCATCAAGCAACCCATACCTGGCTTCGAGCGATGATGGCC
13032	(1106)	CAGACCCATCAAGCAACCCATACCTGGCTTCGAGCGATGATGGCC
CEFgInA1	(1106)	CGGACCCATCCGGCAACCCATACCTGGCTTCGAGCGATGATGGCC
CEFgInA2	(1118)	CGGACCCATCCGGTAAACCCATACCTGGCTTCGAGCGATGATGGCC
MtugInA2	(1019)	GTGATTGGCTGCAATTCCATATCTCAATTGGCCCTGCTGCTCGCCGG
MtugInA3	(1022)	TGGACCCCTGGGCAACCCATACCTGGCTTCGAGCGATGGACTG
MtugInA4	(1070)	CGGGGGGTGATGTCACCAAGTACCTGGGGGTGGGGGCTCTCAATTGCTGGA
MtugInA1	(1109)	CGGACTCTGGGGCAACCCGATCTGGCTTCGAGCGATGATGGCA
Consensus	(1151)	C GACCC TCGGGCAACCC TACCTGGCTTCG GCGATGATGGCA
	1201	
2247	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGGTCCAGTGGACAA
13032	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGGTCCAGTGGACAA
CEFgInA1	(1156)	GGCCTGGACGGTGTGAAGAACCGCATCGAGCCACACGGTCCAGTGGACAA
CEFgInA2	(1168)	GGCCTGGACGGCATCCGAACCGCATCGAACCCGACGGCCCTCTGGACAA
MtugInA2	(1069)	GGATTGGGGGTGAGAGAAGGGTAACTGGCTGGGCCGGAGCGAGGA
MtugInA3	(1072)	GCACCTGACGGCATGAAGAACCGAGGGCTGGTGGCGTGGAAACGACCGT
MtugInA4	(1120)	GGGTGTCACGGTATCGACGGGGCTTCAGCTGGCCGGGGCTGTGCTGG
MtugInA1	(1159)	GGCCTGGACGGTATCAAGAACAGATCGAGCCGCAGGGCCCGTGGACAA
Consensus	(1201)	GGCCTGGACGGTATCAAGAACCGCATCGAGCCGCAGGGCCGGCC GTGGACAA
	1251	
2247	(1206)	GGACCTCTACGAACCTGGACCGAGAGGAAGCTGCATCCAT-----TCCAC
13032	(1206)	GGACCTCTACGAACCTGGACCGAGAGGAAGCTGCATCCAT-----TCCAC
CEFgInA1	(1206)	GGACCTCTACGGAGCTCCACCGAGAGGAAGCTGCATCCAT-----CCCGC
CEFgInA2	(1218)	GGACCTCTATGAGCTCCCCCGAGGGAGCTGGCATCCAT-----GGCCG
	1300	

Mtu	InA2	(1119)	CAACGTATGGGACCTCACACCCGAGGAACGCCAGCGATGGGTAACCGAG
Mtu	InA3	(1122)	AGACCCGACACAGCTGTCTGACGTGGATCGCTGACCGTGCCGGCATTCTGC
Mtu	InA4	(1170)	CAAGG-----CCT-----ACC-----AAGGCGCCGATGU-----CGAAC
Mtu	InA1	(1209)	GGATCTCTACGAGCTCCGGCGGAAGAGGCCCGAGT-----CCCCC
Consensus		(1251)	GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT CCCAC
		1301	1350
2247		(1250)	AGGCACCAACCTCCCTGGAAAGCATCCCTGAAGGCACTGCAGGAAGACACC
13032		(1250)	AGGCACCAACCTCCCTGGAAAGCATCCCTGAAGGCACTGCAGGAAGACACC
CEFgInA1		(1250)	AGGCACCGACCTCCCTGGAGGATCCCTGAAGGCCCTGCAGGGAGGACTCC
CEFgInA2		(1262)	AGGCCCCCACCTGACCTGGAAACAGGGCTGAAAGGCCCTGGAGGAGGACAC
Mtu	InA2	(1169)	AATTGGCGTCCAGTTGGATAGTGGCTGGCGCCATGGAGGC-----CTCC
Mtu	InA3	(1172)	GACTTGGTGCGGATGAGGCGGATGCAAATGCTGTACTGGATAG-----TTC
Mtu	InA4	(1199)	GGCTGCGGGTTAACCTGGCCGACGCCGCGGTTGCTGTTGAGGA-----TCT
Mtu	InA1	(1253)	AGACTCCGACCCCACCTGTCAGAATGTGAATCGACCGTCTCGAGGCCGACAC
Consensus		(1301)	AGGC CGGACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC
		1351	1400
2247		(1300)	GACCTCCCTCACCGAGTCTGACGTCTCACCGAGGATCTCATCGA-GGGCT
13032		(1300)	GACCTCCCTCACCGAGTCTGACGTCTCACCGAGGATCTCATCGA-GGGCT
CEFgInA1		(1300)	GACTTCCCTCACCGAGTCCGACGTGTTACCGAGGACCTCATCGA-GGGCT
CEFgInA2		(1312)	GAGCTCCCTCACCGAGGAGTACCGTGTCTCACCGATGATCTCATCGA-GGGCT
Mtu	InA2	(1216)	GAACCTGGTGGAG-----GCCTTGGGGAGCACGTTTTGA-CTTT
Mtu	InA3	(1218)	GAAACTGCTTGGGT-----CATCCCTGGCGATCCCGTGGTAGATGCCGT
Mtu	InA4	(1246)	GCGCTGGTGGCGGAG-----CGCTTGGCGAGGATGUTGTCGCC-GCACU
Mtu	InA1	(1303)	GAATACCTCACCGAAGGAGGGTGTCAACAAACGACCTGATCGA-GACCT
Consensus		(1351)	GA TTCCCTCACCGAG GACGTGTTCACCGAGGATCTCATCGA GGGCT
		1401	1450
2247		(1349)	ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCCAGTTCGGCTGCGC
13032		(1349)	ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCCAGTTCGGCTGCGC
CEFgInA1		(1349)	ACATCCAGTACAAGTAC-----GACAACGAGATCACCCCGTCCGGCTGCGC
CEFgInA2		(1361)	ATGTCGCCTACAAGCAT-----GAAACATGAGATCACCCCGTGGCGTCTGCGC
Mtu	InA2	(1259)	TCTTGGCGAACAAAGCGCACGGAGTGGCGAACATACCGCAGCCACGTACG
Mtu	InA3	(1263)	GGTCGGGTACGCCAGT-TAGAGCATGAGCCGTAC-----GGTGACCTCGAT
Mtu	InA4	(1289)	ACCTGAACAAAGCGCGGTGTGGAGCTGGCGGGCTCAACCGGGGGICA-----
Mtu	InA1	(1352)	GGATCAGTTCAACCGC-----GAAAACCGAGATGAGGCCGTCACAACTCCG
Consensus		(1401)	ACATGCACTACAAGCGC GA AACGAGATCTCCCC GT CGGCTGCGC
		1451	1495
2247		(1396)	CCAACCCCGCAGGAATTGAAATTGTACTTCGACTGC-----
13032		(1396)	CCAACCCCGCAGGAATTGAAATTGTACTTCGACTGCTAA-----
CEFgInA1		(1396)	CCCACCCCGCAGGAATTGAAATTGTACTTCGACTGCTA-----
CEFgInA2		(1408)	CCCACCGCTCTGGATTTGAGCTGACTACCGACTGCTAG-----
Mtu	InA2	(1309)	CCATAACGAGCTCCGACCTACCTGTCGCTGTAG-----
Mtu	InA3	(1309)	CCTGGCGCAGCTCCCGAACAGTCCGGATGCTTGGAGTGTGTA-----
Mtu	InA4	(1337)	CCGATTGGGAGACCATACGTGGATTTGAGGCCGCTCTAG-----
Mtu	InA1	(1399)	CCGGCATCCCTACGAATTGGCGCTGTACTACGACGTTAA-----
Consensus		(1451)	CC ACCCCCGCAGGAATTGAGCTGACTTCGACTGCTA

2247 : *B. flavum* ATCC14067

13032: *C. glutamicum* ATCC13032

CEF: *C. efficiens* YS314

Mtu: *Mycobacterium tuberculosis* H37RV